



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1112210329-25674-188551179453.BLASTQ4

Query=

(33 letters)

Database: All non-redundant GenBank CDS

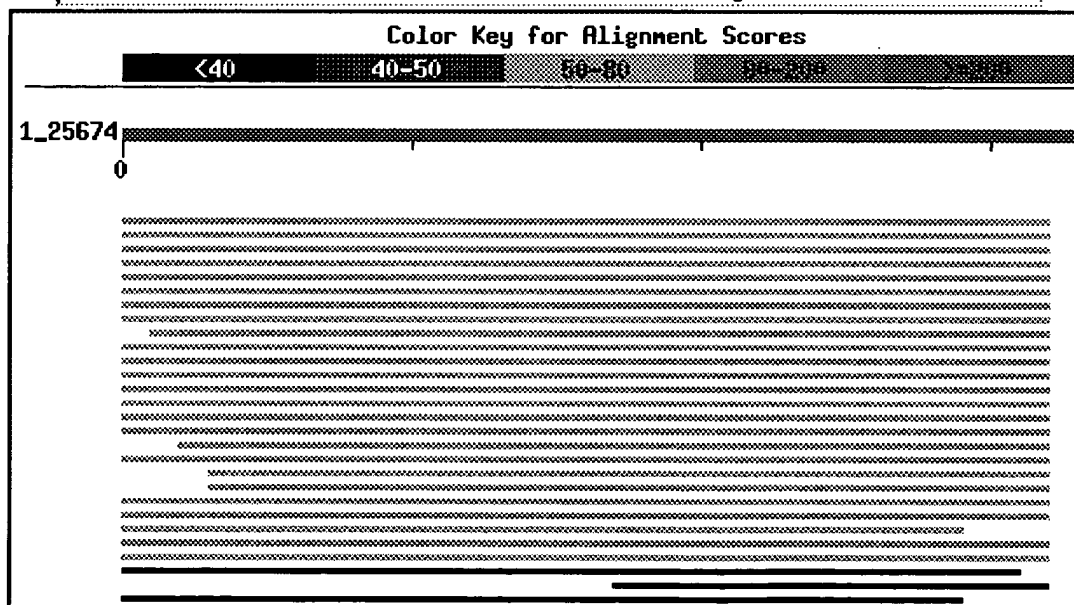
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,408,643 sequences; 815,228,232 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 28 Blast Hits on the Query Sequence






















Mouse-over to show define and scores. Click to show alignments



[Related Structures](#)





Sequences producing significant alignments:

Score E
(bits) Value

gi 4506267 ref NP_000306.1 	parathyroid hormone preproprote...	60	2e-08	
gi 565142 gb AAB31748.1 	human parathyroid hormone; hPTH [s...	60	2e-08	
gi 10120515 pdb 1ET1 B	Chain B, Crystal Structure Of Human ...	60	2e-08	
gi 55635601 ref XP_521846.1 	PREDICTED: similar to Parathyr...	60	2e-08	
gi 7416876 gb AAF62347.1 	parathyroid hormone [Equus caballus]	60	2e-08	
gi 1065314 pdb 1HPH 	Human Parathyroid Hormone Fragment 1 ...	60	2e-08	
gi 5359716 gb AAD42777.1 	parathyroid hormone precursor [Ma...	60	2e-08	
gi 6980561 pdb 1BWV 	The Solution Structure Of Human Parat...	60	2e-08	
gi 1942097 pdb 1ZWB 	Structure Of Human Parathyroid Hormon...	58	6e-08	
gi 50979128 ref NP_001003302.1 	parathyroid hormone [Canis ...	58	8e-08	
gi 47523856 ref NP_999566.1 	parathyroid hormone [Sus scrof...	58	8e-08	
gi 85 emb CAA23439.1 	preproparathyroid hormone [Bos taurus...	57	2e-07	
gi 57163745 ref NP_001009210.1 	parathyroid hormone [Felis ...	57	2e-07	
gi 1942098 pdb 1ZWC 	Structure Of Bovine Parathyroid Hormo...	57	2e-07	
gi 1942099 pdb 1ZWD 	Structure Of Human Parathyroid Hormon...	57	2e-07	
gi 163647 gb AAA30749.1 	preproparathyroid hormone	57	2e-07	
gi 229314 prf 701028A	parathyrin	57	2e-07	
gi 2624852 pdb 1HTH 	The Solution Structure Of Cyclic Huma...	56	3e-07	
gi 2392656 pdb 1ZWG 	Succinyl Human Parathyroid Hormone 4-...	55	5e-07	
gi 1942100 pdb 1ZWE 	Structure Of Human Parathyroid Hormon...	55	5e-07	
gi 8394100 ref NP_058740.1 	parathyroid hormone [Rattus nor...	53	2e-06	
gi 11513553 pdb 1FVY A	Chain A, Solution Structure Of The O...	53	2e-06	
gi 30387856 gb AAP32220.1 	hypothalamic parathyroid hormone...	53	2e-06	
gi 10181174 ref NP_065648.1 	parathyroid hormone [Mus muscu...	51	1e-05	
gi 601933 gb AAA57156.1 	parathyroid hormone precursor [Rat...	50	2e-05	
gi 45382055 ref NP_990783.1 	thyroid hormone [Gallus gallus...	41	0.008	
gi 208546 gb AAA72765.1 	parathyroid hormone	37	0.11	
gi 34499964 gb AAQ73561.1 	parathyroid hormone type-2 precu...	32	6.2	

Alignments


Get selected sequences Select all Deselect all

☒ >[gi|4506267|ref|NP_000306.1|](#)  parathyroid hormone preproprotein [Homo sapiens]
[gi|2144647|pir|PTHU](#) parathyroid hormone precursor [validated] - human
[gi|37144|emb|CAA23843.1|](#)  unnamed protein product [Homo sapiens]
[gi|190704|gb|AAA60215.1|](#)  preproparathyroid hormone
[gi|131547|sp|P01270|PTHY_HUMAN](#)  Parathyroid hormone precursor (Parathyrin) (PTH)
Length = 115

Score = 59.7 bits (143), Expect = 2e-08

Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)






Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 32 SVSEIQIMHNLGKHLNSMERVEWLRKKLQDVHNF 65

 >[gi|565142|gb|AAB31748.1|](#) human parathyroid hormone; hPTH [synthetic construct]
[gi|209186|gb|AAA73011.1|](#) parathyroid hormone
Length = 85

Score = 59.7 bits (143), Expect = 2e-08

Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)



Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 2 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 35

 >[gi|10120515|pdb|1ET1|B](#)  Chain B, Crystal Structure Of Human Parathyroid Hormone
0.9 A Resolution
[gi|10120514|pdb|1ET1|A](#)  Chain A, Crystal Structure Of Human Parathyroid Hormone
0.9 A Resolution
[gi|1942096|pdb|1ZWA|](#)  Structure Of Human Parathyroid Hormone Fragment 1-34, Nmr
Structures
[gi|6980572|pdb|1HPY|](#)  The Solution Structure Of Human Parathyroid Hormone' Fragm
In 20% Trifluorethanol, Nmr, 10 Structures
Length = 34

Score = 59.7 bits (143), Expect = 2e-08

Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)


Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

 >[gi|55635601|ref|XP_521846.1|](#)  PREDICTED: similar to Parathyroid hormone precursor
(PTH) (Parathormone) [Pan troglodytes]
Length = 147

Score = 59.7 bits (143), Expect = 2e-08

Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)



Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 64 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 97

 >[gi|7416876|gb|AAF62347.1|](#) parathyroid hormone [Equus caballus]
Length = 86

Score = 59.7 bits (143), Expect = 2e-08


Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 3 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 36

 >[gi|1065314|pdb|1HPH|](#)  Human Parathyroid Hormone Fragment 1 - 37 (Hpth(1-37))
Structures)
Length = 37



Score = 59.7 bits (143), Expect = 2e-08
Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

 >[gi|5359716|gb|AAD42777.1|](#) parathyroid hormone precursor [Macaca fascicularis]
[gi|13124462|sp|Q9XT35|PTHY_MACFA](#) Parathyroid hormone precursor (Parathyrin) (PTH)
Length = 115



Score = 59.7 bits (143), Expect = 2e-08
Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 65

 >[gi|6980561|pdb|1BWV|](#)  The Solution Structure Of Human Parathyroid Hormone Fra
1-39, Nmr, 10 Structures
Length = 39





Score = 59.7 bits (143), Expect = 2e-08
Identities = 29/34 (85%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

 >[gi|1942097|pdb|1ZWV|](#)  Structure Of Human Parathyroid Hormone Fragment 2-37, N
Structures
Length = 36




Score = 58.2 bits (139), Expect = 6e-08
Identities = 28/33 (84%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 2 VSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
VSEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 33

 >[gi|50979128|ref|NP_001003302.1|](#)  parathyroid hormone [Canis familiaris]
[gi|1085421|pir||JC4202](#) parathyroid hormone precursor - dog
[gi|558916|gb|AAA82584.1|](#)  parathyroid hormone precursor
[gi|1709894|sp|P52212|PTHY_CANFA](#)  Parathyroid hormone precursor (Parathyrin) (PTH)
Length = 115






Score = 57.8 bits (138), Expect = 8e-08
 Identities = 28/34 (82%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
 SVSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
 Sbjct: 32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 65

>[gi|47523856|ref|NP_999566.1|](#)  [parathyroid hormone \[Sus scrofa\]](#)
[gi|2144646|pir||PTPG](#) parathyroid hormone precursor - pig
[gi|1839|emb|CAA29193.1|](#)  unnamed protein product [Sus scrofa]
[gi|131548|sp|P01269|PTHY_PIG](#)  Parathyroid hormone precursor (Parathyrin) (PTH)
 Length = 115




Score = 57.8 bits (138), Expect = 8e-08
 Identities = 28/34 (82%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
 SVSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
 Sbjct: 32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDVHNF 65

>[gi|85|emb|CAA23439.1|](#)  preproparathyroid hormone [Bos taurus]
[gi|31982386|ref|NP_776379.2|](#)  parathyroid hormone [Bos taurus]
[gi|69233|pir||PTBO](#) parathyroid hormone precursor - bovine
[gi|163645|qb|AAA30748.1|](#)  preproparathyroid hormone
[gi|163643|qb|AAA30747.1|](#)  preproparathyroid hormone
[gi|131545|sp|P01268|PTHY_BOVIN](#)  Parathyroid hormone precursor (Parathyrin) (PTH)
 Length = 115


Score = 56.6 bits (135), Expect = 2e-07
 Identities = 27/34 (79%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
 +VSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
 Sbjct: 32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 65

>[gi|57163745|ref|NP_001009210.1|](#)  parathyroid hormone [Felis catus]
[gi|11119195|qb|AAG30545.1|](#)  preproparathyroid hormone [Felis catus]
[gi|47117317|sp|Q9GL67|PTHY_FELCA](#)  Parathyroid hormone precursor (Parathyrin) (PT)
 Length = 115

Score = 56.6 bits (135), Expect = 2e-07
 Identities = 27/34 (79%), Positives = 30/34 (88%), Gaps = 1/34 (2%)



Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
 SVSEIQ HN GKHL+S ERVEWLR+KLQDVHN+
 Sbjct: 32 SVSEIQFMHNLGKHLSSVERVEWLRKKLQDVHNF 65

>[gi|1942098|pdb|1ZWC|](#)  Structure Of Bovine Parathyroid Hormone Fragment 1-37,

Structures
Length = 37

Score = 56.6 bits (135), Expect = 2e-07
Identities = 27/34 (79%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
+VSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
Sbjct: 1 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 34

 >[gi|1942099|pdb|1ZWD|](#)  Structure Of Human Parathyroid Hormone Fragment 3-37, 1
Structures
Length = 35


Score = 56.6 bits (135), Expect = 2e-07
Identities = 27/32 (84%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 3 SEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SEIQ HN GKHLNS ERVEWLRKKLQDVHN+
Sbjct: 1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 32

 >[gi|163647|qb|AAA30749.1|](#)  preproparathyroid hormone
Length = 115



Score = 56.6 bits (135), Expect = 2e-07
Identities = 27/34 (79%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
+VSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
Sbjct: 32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 65

 >[gi|229314|prf||701028A](#) parathyrin
Length = 84




Score = 56.6 bits (135), Expect = 2e-07
Identities = 27/34 (79%), Positives = 30/34 (88%), Gaps = 1/34 (2%)

Query: 1 SVSEIQ-CHNCGKHLNSXERVEWLRKKLQDVHNY 33
+VSEIQ HN GKHL+S ERVEWLRKKLQDVHN+
Sbjct: 1 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 34

 >[gi|2624852|pdb|1HTH|](#)  The Solution Structure Of Cyclic Human Parathyroid Hormone
Fragment 1 - 34, Nmr, 10 Structures
Length = 34



Score = 55.8 bits (133), Expect = 3e-07
Identities = 28/34 (82%), Positives = 29/34 (85%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
SVSEIQ HN G HLN ERVEWLRKKLQDVHN+
Sbjct: 1 SVSEIQLXHNLGXHLNEXERVEWLRKKLQDVHNF 34

 >[gi|2392656|pdb|1ZWG|](#)  Succinyl Human Parathyroid Hormone 4-37, Nmr, 10 Struct
[gi|2392655|pdb|1ZWF|](#)  Structure Of N-Terminal Acetylated Human Parathyroid Horm
 Nmr, 10 Structures
 Length = 35






Score = 55.1 bits (131), Expect = 5e-07
 Identities = 26/31 (83%), Positives = 27/31 (87%), Gaps = 1/31 (3%)

Query: 4 EIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
 EIQ HN GKHLNS ERVEWLRKKLQDVHN+
 Sbjct: 2 EIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 32

 >[gi|1942100|pdb|1ZWE|](#)  Structure Of Human Parathyroid Hormone Fragment 4-37, N
 Structures
 Length = 34



Score = 55.1 bits (131), Expect = 5e-07
 Identities = 26/31 (83%), Positives = 27/31 (87%), Gaps = 1/31 (3%)

Query: 4 EIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
 EIQ HN GKHLNS ERVEWLRKKLQDVHN+
 Sbjct: 1 EIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 31

 >[gi|8394100|ref|NP_058740.1|](#)  parathyroid hormone [Rattus norvegicus]
[gi|56003|emb|CAA29192.1|](#)  unnamed protein product [Rattus norvegicus]
[gi|92588|pir|A05091](#) parathyroid hormone precursor - rat
[gi|206485|gb|AAA41979.1|](#)  preproparathyroid hormone
[gi|131549|sp|P04089|PTHY RAT](#)  Parathyroid hormone precursor (Parathyrin) (PTH)
 Length = 115



Score = 53.1 bits (126), Expect = 2e-06
 Identities = 25/34 (73%), Positives = 29/34 (85%), Gaps = 1/34 (2%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
 +VSEIQ HN GKHL S ER++WLRKKLQDVHN+
 Sbjct: 32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDVHNF 65

 >[gi|11513553|pdb|1FVY|A](#)  Chain A, Solution Structure Of The Osteogenic 1-31 Fra
 The Human Parathyroid Hormone
 Length = 31

Score = 53.1 bits (126), Expect = 2e-06
 Identities = 27/31 (87%), Positives = 27/31 (87%), Gaps = 1/31 (3%)




Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDV 30
 SVSEIQ HN GKHLNS ERVEWLRKKLQDV
 Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

 >[gi|30387856|gb|AAP32220.1|](#)  hypothalamic parathyroid hormone [Rattus norvegicus]
Length = 105

Score = 53.1 bits (126), Expect = 2e-06

Identities = 25/34 (73%), Positives = 29/34 (85%), Gaps = 1/34 (2%)


Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
+VSEIQ HN GKHL S ER++WLRKKLQDVHN+
Sbjct: 22 AVSEIQLMHNLGKHLASVERMQWLRKKLQDVHNF 55

 >[gi|10181174|ref|NP_065648.1|](#)  parathyroid hormone [Mus musculus]
[gi|4092930|gb|AAC99656.1|](#)  parathyroid hormone precursor [Mus musculus]
Length = 115

Score = 50.8 bits (120), Expect = 1e-05

Identities = 23/34 (67%), Positives = 29/34 (85%), Gaps = 1/34 (2%)






Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
+VSEIQ HN GKHL S ER++WLR+KLQD+HN+
Sbjct: 32 AVSEIQLMHNLGKHLASMERMQWLRKKLQDMHNF 65

 >[gi|601933|gb|AAA57156.1|](#) parathyroid hormone precursor [Rattus norvegicus]
[gi|2118603|pir||I51851](#) parathyroid hormone - rat (fragment)
Length = 105

Score = 50.1 bits (118), Expect = 2e-05

Identities = 23/34 (67%), Positives = 28/34 (82%), Gaps = 1/34 (2%)


Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHNY 33
++SEIQ HN GKHL S ER++WLRKKLQD HN+
Sbjct: 22 AISEIQLMHNLGKHLASVERMQWLRKKLQDGHNF 55

 >[gi|45382055|ref|NP_990783.1|](#)  thyroid hormone [Gallus gallus]
[gi|212592|gb|AAB02866.1|](#)  parathyroid hormone precursor [Gallus gallus]
[gi|86411|pir||A34937](#) parathyroid hormone precursor - chicken
[gi|212768|gb|AAA49093.1|](#)  thyroid hormone precursor
[gi|131546|sp|P15743|PTHY_CHICK](#)  Parathyroid hormone precursor (PTH)
Length = 119

Score = 41.2 bits (95), Expect = 0.008

Identities = 19/33 (57%), Positives = 26/33 (78%), Gaps = 1/33 (3%)


Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDVHN 32
SVSE+Q HN G+H ++ ER +WL+ KLQDVH+
Sbjct: 32 SVSEMQLMHNLGHRHTVERQDWLQMKLQDVHS 64

 >[gi|208546|gb|AAA72765.1|](#) parathyroid hormone

Length = 67

Score = 37.4 bits (85), Expect = 0.11
Identities = 15/16 (93%), Positives = 16/16 (100%)

Query: 18 ERVEWLRKKLQDVHNY 33
 ERVEWLRKKLQDVHN+
Sbjct: 2 ERVEWLRKKLQDVHNF 17

 >gi|34499964|gb|AAQ73561.1| parathyroid hormone type-2 precursor [Takifugu rubri
Length = 91

Score = 31.6 bits (70), Expect = 6.2
Identities = 14/31 (45%), Positives = 22/31 (70%), Gaps = 1/31 (3%)

Query: 1 SVSEIQC-HNCGKHLNSXERVEWLRKKLQDV 30
 ++SE+Q HN +H ER +WL++KL+DV
Sbjct: 30 TISEVQLMHNVREHKQVGERQDWLQEKLKDV 60

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Mar 27, 2005 1:57 AM
Number of letters in database: 815,228,232
Number of sequences in database: 2,408,643

Lambda	K	H
0.318	0.131	0.427

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12,595,323

Number of Sequences: 2408643

Number of extensions: 204760

Number of successful extensions: 1200

Number of sequences better than 10.0: 12

Number of HSP's better than 10.0 without gapping: 11

Number of HSP's successfully gapped in prelim test: 1

Number of HSP's that attempted gapping in prelim test: 1189

Number of HSP's gapped (non-prelim): 12

length of query: 33

length of database: 815,228,232

effective HSP length: 8

effective length of query: 25

effective length of database: 795,959,088

effective search space: 19898977200

effective search space used: 19898977200

T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 69 (31.2 bits)